

Eric E Schadt

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/6172599/eric-e-schadt-publications-by-year.pdf>

Version: 2024-04-27

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

297
papers

47,034
citations

90
h-index

216
g-index

326
ext. papers

58,814
ext. citations

14.4
avg, IF

6.89
L-index

#	Paper	IF	Citations
297	A mechanistic framework for cardiometabolic and coronary artery diseases 2022 , 1, 85-100		5
296	Targeted Next-Generation Sequencing Reveals Exceptionally High Rates of Molecular Driver Mutations in Never-Smokers With Lung Adenocarcinoma.. <i>Oncologist</i> , 2022 ,	5.7	2
295	Integrative network analysis of early-stage lung adenocarcinoma identifies aurora kinase inhibition as interceptor of invasion and progression.. <i>Nature Communications</i> , 2022 , 13, 1592	17.4	1
294	An integrated taxonomy for monogenic inflammatory bowel disease. <i>Gastroenterology</i> , 2021 ,	13.3	4
293	A Drosophila platform identifies a novel, personalized therapy for a patient with adenoid cystic carcinoma. <i>iScience</i> , 2021 , 24, 102212	6.1	4
292	Rare Germline Pathogenic Variants Identified by Multigene Panel Testing and the Risk of Aggressive Prostate Cancer. <i>Cancers</i> , 2021 , 13,	6.6	1
291	Bayesian Model Infers Drug Repurposing Candidates for Treatment of COVID-19. <i>Applied Sciences (Switzerland)</i> , 2021 , 11, 2466	2.6	0
290	Haploinsufficiency of POU4F1 causes an ataxia syndrome with hypotonia and intention tremor. <i>Human Mutation</i> , 2021 , 42, 685-693	4.7	
289	Discovery and fine-mapping of height loci via high-density imputation of GWASs in individuals of African ancestry. <i>American Journal of Human Genetics</i> , 2021 , 108, 564-582	11	7
288	Myeloid Cell-associated Resistance to PD-1/PD-L1 Blockade in Urothelial Cancer Revealed Through Bulk and Single-cell RNA Sequencing. <i>Clinical Cancer Research</i> , 2021 , 27, 4287-4300	12.9	9
287	A composite biomarker of neutrophil-lymphocyte ratio and hemoglobin level correlates with clinical response to PD-1 and PD-L1 inhibitors in advanced non-small cell lung cancers. <i>BMC Cancer</i> , 2021 , 21, 441	4.8	7
286	Phenotyping of clinical trial eligibility text from cancer studies into computable criteria in electronic health records.. <i>Journal of Clinical Oncology</i> , 2021 , 39, 6592-6592	2.2	
285	Detecting and phasing minor single-nucleotide variants from long-read sequencing data. <i>Nature Communications</i> , 2021 , 12, 3032	17.4	6
284	Extracting longitudinal anticancer treatments at scale using deep natural language processing and temporal reasoning.. <i>Journal of Clinical Oncology</i> , 2021 , 39, e18747-e18747	2.2	
283	Analyzing treatment patterns and time to the next treatment in chronic lymphocytic leukemia real-world data using automated temporal phenotyping.. <i>Journal of Clinical Oncology</i> , 2021 , 39, e19512- e19512 ^{2219512⁰}		
282	Continuous genomic monitoring of multiple myeloma patients to identify patients of high risk for poor prognosis.. <i>Journal of Clinical Oncology</i> , 2021 , 39, e20035-e20035	2.2	
281	Effect of APOE and a polygenic risk score on incident dementia and cognitive decline in a healthy older population. <i>Aging Cell</i> , 2021 , 20, e13384	9.9	3

280	IL10RB as a key regulator of COVID-19 host susceptibility and severity 2021 ,		2
279	Genetic variants associated with inherited cardiovascular disorders among 13,131 asymptomatic older adults of European descent. <i>Npj Genomic Medicine</i> , 2021 , 6, 51	6.2	3
278	Genomic Risk Prediction for Breast Cancer in Older Women. <i>Cancers</i> , 2021 , 13,	6.6	1
277	Intestinal Inflammation Modulates the Expression of ACE2 and TMPRSS2 and Potentially Overlaps With the Pathogenesis of SARS-CoV-2-related Disease. <i>Gastroenterology</i> , 2021 , 160, 287-301.e20	13.3	50
276	Transformative Network Modeling of Multi-omics Data Reveals Detailed Circuits, Key Regulators, and Potential Therapeutics for Alzheimer's Disease. <i>Neuron</i> , 2021 , 109, 257-272.e14	13.9	29
275	A Noncoding Variant Near PPP1R3B Promotes Liver Glycogen Storage and MetS, but Protects Against Myocardial Infarction. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2021 , 106, 372-387	5.6	3
274	Network study of nasal transcriptome profiles reveals master regulator genes of asthma. <i>Journal of Allergy and Clinical Immunology</i> , 2021 , 147, 879-893	11.5	8
273	AKI in Hospitalized Patients with COVID-19. <i>Journal of the American Society of Nephrology: JASN</i> , 2021 , 32, 151-160	12.7	225
272	Molecular subtyping of Alzheimer's disease using RNA sequencing data reveals novel mechanisms and targets. <i>Science Advances</i> , 2021 , 7,	14.3	39
271	An integrative multiomic network model links lipid metabolism to glucose regulation in coronary artery disease. <i>Nature Communications</i> , 2021 , 12, 547	17.4	12
270	Polygenic risk score for alcohol drinking behavior improves prediction of inflammatory bowel disease risk. <i>Human Molecular Genetics</i> , 2021 , 30, 514-523	5.6	0
269	A Molecular network approach reveals shared cellular and molecular signatures between chronic fatigue syndrome and other fatiguing illnesses 2021 ,		2
268	A proteogenomic portrait of lung squamous cell carcinoma. <i>Cell</i> , 2021 , 184, 4348-4371.e40	56.2	15
267	Downregulation of exhausted cytotoxic T cells in gene expression networks of multisystem inflammatory syndrome in children. <i>Nature Communications</i> , 2021 , 12, 4854	17.4	12
266	Prognostic value of polygenic risk scores for adults with psychosis. <i>Nature Medicine</i> , 2021 , 27, 1576-1581	50.5	7
265	Molecular Characterization of Limited Ulcerative Colitis Reveals Novel Biology and Predictors of Disease Extension. <i>Gastroenterology</i> , 2021 , 161, 1953-1968.e15	13.3	2
264	Deep Analysis of the Peripheral Immune System in IBD Reveals New Insight in Disease Subtyping and Response to Monotherapy or Combination Therapy. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2021 , 12, 599-632	7.9	2
263	Population-based estimates of breast cancer risk for carriers of pathogenic variants identified by gene-panel testing. <i>Npj Breast Cancer</i> , 2021 , 7, 153	7.8	1

262	A consensus proteomic analysis of Alzheimer's disease brain and cerebrospinal fluid reveals early changes in energy metabolism associated with microglia and astrocyte activation. <i>Alzheimer's and Dementia</i> , 2020 , 16, e039504	1.2	
261	Familial Hypercholesterolemia in a Healthy Elderly Population. <i>Circulation Genomic and Precision Medicine</i> , 2020 , 13, e002938	5.2	2
260	A reference profile-free deconvolution method to infer cancer cell-intrinsic subtypes and tumor-type-specific stromal profiles. <i>Genome Medicine</i> , 2020 , 12, 24	14.4	12
259	Genomic analyses implicate noncoding de novo variants in congenital heart disease. <i>Nature Genetics</i> , 2020 , 52, 769-777	36.3	33
258	Medically actionable pathogenic variants in a population of 13,131 healthy elderly individuals. <i>Genetics in Medicine</i> , 2020 , 22, 1883-1886	8.1	10
257	Systems modeling of white matter microstructural abnormalities in Alzheimer's disease. <i>NeuroImage: Clinical</i> , 2020 , 26, 102203	5.3	5
256	Intratumoral heterogeneity and clonal evolution in liver cancer. <i>Nature Communications</i> , 2020 , 11, 291	17.4	102
255	Altering Sphingolipid Metabolism Attenuates Cell Death and Inflammatory Response After Myocardial Infarction. <i>Circulation</i> , 2020 , 141, 916-930	16.7	32
254	VGF-derived peptide TLQP-21 modulates microglial function through C3aR1 signaling pathways and reduces neuropathology in 5xFAD mice. <i>Molecular Neurodegeneration</i> , 2020 , 15, 4	19	27
253	Comparison of brain connectomes by MRI and genomics and its implication in Alzheimer's disease. <i>BMC Medicine</i> , 2020 , 18, 23	11.4	1
252	Large-scale proteomic analysis of Alzheimer's disease brain and cerebrospinal fluid reveals early changes in energy metabolism associated with microglia and astrocyte activation. <i>Nature Medicine</i> , 2020 , 26, 769-780	50.5	226
251	Integrative study of the upper and lower airway microbiome and transcriptome in asthma. <i>JCI Insight</i> , 2020 , 5,	9.9	19
250	Predictive network modeling in human induced pluripotent stem cells identifies key driver genes for insulin responsiveness. <i>PLoS Computational Biology</i> , 2020 , 16, e1008491	5	7
249	Machine Learning to Predict Mortality and Critical Events in a Cohort of Patients With COVID-19 in New York City: Model Development and Validation. <i>Journal of Medical Internet Research</i> , 2020 , 22, e24018	7.6	82
248	Lessons learned from expanded reproductive carrier screening in self-reported Ashkenazi, Sephardi, and Mizrahi Jewish patients. <i>Molecular Genetics & Genomic Medicine</i> , 2020 , 8, e1053	2.3	9
247	A New Liver Expression Quantitative Trait Locus Map From 1,183 Individuals Provides Evidence for Novel Expression Quantitative Trait Loci of Drug Response, Metabolic, and Sex-Biased Phenotypes. <i>Clinical Pharmacology and Therapeutics</i> , 2020 , 107, 1383-1393	6.1	10
246	Dual transcriptomic and epigenomic study of reaction severity in peanut-allergic children. <i>Journal of Allergy and Clinical Immunology</i> , 2020 , 145, 1219-1230	11.5	21
245	Very Early Onset Inflammatory Bowel Disease: A Clinical Approach With a Focus on the Role of Genetics and Underlying Immune Deficiencies. <i>Inflammatory Bowel Diseases</i> , 2020 , 26, 820-842	4.5	40

244	Epigenomic characterization of <i>Clostridioides difficile</i> finds a conserved DNA methyltransferase that mediates sporulation and pathogenesis. <i>Nature Microbiology</i> , 2020 , 5, 166-180	26.6	36
243	Sex differences in human adipose tissue gene expression and genetic regulation involve adipogenesis. <i>Genome Research</i> , 2020 , 30, 1379-1392	9.7	9
242	Aberrant methylation underlies insulin gene expression in human insulinoma. <i>Nature Communications</i> , 2020 , 11, 5210	17.4	2
241	Large eQTL meta-analysis reveals differing patterns between cerebral cortical and cerebellar brain regions. <i>Scientific Data</i> , 2020 , 7, 340	8.2	26
240	Meta-Analysis of the Alzheimer's Disease Human Brain Transcriptome and Functional Dissection in Mouse Models. <i>Cell Reports</i> , 2020 , 32, 107908	10.6	68
239	Integrated Proteogenomic Characterization across Major Histological Types of Pediatric Brain Cancer. <i>Cell</i> , 2020 , 183, 1962-1985.e31	56.2	45
238	Multiscale causal networks identify VGF as a key regulator of Alzheimer's disease. <i>Nature Communications</i> , 2020 , 11, 3942	17.4	28
237	Sampling the host response to SARS-CoV-2 in hospitals under siege. <i>Nature Medicine</i> , 2020 , 26, 1157-1158	50.5	8
236	An inflammatory cytokine signature predicts COVID-19 severity and survival. <i>Nature Medicine</i> , 2020 , 26, 1636-1643	50.5	895
235	Human geroprotector discovery by targeting the converging subnetworks of aging and age-related diseases. <i>GeroScience</i> , 2020 , 42, 353-372	8.9	24
234	Prevalence and disease predisposition of p.A91V perforin in an aged population of European ancestry. <i>Blood</i> , 2020 , 135, 582-584	2.2	2
233	Integrative transcriptome imputation reveals tissue-specific and shared biological mechanisms mediating susceptibility to complex traits. <i>Nature Communications</i> , 2019 , 10, 3834	17.4	28
232	Single-Cell Analysis of Crohn's Disease Lesions Identifies a Pathogenic Cellular Module Associated with Resistance to Anti-TNF Therapy. <i>Cell</i> , 2019 , 178, 1493-1508.e20	56.2	219
231	Discovering genetic interactions bridging pathways in genome-wide association studies. <i>Nature Communications</i> , 2019 , 10, 4274	17.4	26
230	A Network Analysis of Multiple Myeloma Related Gene Signatures. <i>Cancers</i> , 2019 , 11,	6.6	16
229	Functional interpretation of genetic variants using deep learning predicts impact on chromatin accessibility and histone modification. <i>Nucleic Acids Research</i> , 2019 , 47, 10597-10611	20.1	14
228	Biology and Bias in Cell Type-Specific RNAseq of Nucleus Accumbens Medium Spiny Neurons. <i>Scientific Reports</i> , 2019 , 9, 8350	4.9	11
227	Contribution of Gene Regulatory Networks to Heritability of Coronary Artery Disease. <i>Journal of the American College of Cardiology</i> , 2019 , 73, 2946-2957	15.1	28

226	A personalized platform identifies trametinib plus zoledronate for a patient with KRAS-mutant metastatic colorectal cancer. <i>Science Advances</i> , 2019 , 5, eaav6528	14.3	35
225	ORE identifies extreme expression effects enriched for rare variants. <i>Bioinformatics</i> , 2019 , 35, 3906-3912	7.2	3
224	Predispositional genome sequencing in healthy adults: design, participant characteristics, and early outcomes of the PeopleSeq Consortium. <i>Genome Medicine</i> , 2019 , 11, 10	14.4	22
223	Differential activity of transcribed enhancers in the prefrontal cortex of 537 cases with schizophrenia and controls. <i>Molecular Psychiatry</i> , 2019 , 24, 1685-1695	15.1	20
222	Integrative analysis of loss-of-function variants in clinical and genomic data reveals novel genes associated with cardiovascular traits. <i>BMC Medical Genomics</i> , 2019 , 12, 108	3.7	5
221	Structural variation at the CYP2C locus: Characterization of deletion and duplication alleles. <i>Human Mutation</i> , 2019 , 40, e37-e51	4.7	8
220	Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. <i>Cell</i> , 2019 , 179, 964-983	53.1	173
219	Investigating racial differences in treatment responses through analysis of real-world data (RWD).. <i>Journal of Clinical Oncology</i> , 2019 , 37, e18141-e18141	2.2	
218	Analysis of real-world data (RWD) on treatment (tx) sequencing in patients with advanced non-small cell lung cancer (aNSCLC).. <i>Journal of Clinical Oncology</i> , 2019 , 37, e20642-e20642	2.2	
217	Inching towards precision medicine for multiple myeloma with causal network models.. <i>Journal of Clinical Oncology</i> , 2019 , 37, e19526-e19526	2.2	
216	A phase I study of the safety and immunogenicity of a multi-peptide personalized genomic vaccine in the adjuvant treatment of solid tumors and hematological malignancies.. <i>Journal of Clinical Oncology</i> , 2019 , 37, e14307-e14307	2.2	2
215	Inferring Causal Associations between Genes and Disease via the Mapping of Expression Quantitative Trait Loci 2019 , 697-38		1
214	A Complete Genome Screening Program of Clinical Methicillin-Resistant Staphylococcus aureus Isolates Identifies the Origin and Progression of a Neonatal Intensive Care Unit Outbreak. <i>Journal of Clinical Microbiology</i> , 2019 , 57,	9.7	6
213	High-Throughput Identification of the Plasma Proteomic Signature of Inflammatory Bowel Disease. <i>Journal of Crohn's and Colitis</i> , 2019 , 13, 462-471	1.5	6
212	CDT2-controlled cell cycle reentry regulates the pathogenesis of Alzheimer's disease. <i>Alzheimer's and Dementia</i> , 2019 , 15, 217-231	1.2	17
211	Deciphering bacterial epigenomes using modern sequencing technologies. <i>Nature Reviews Genetics</i> , 2019 , 20, 157-172	30.1	61
210	Integrative approach to sporadic Alzheimer's disease: deficiency of TYROBP in cerebral A β amyloidosis mouse normalizes clinical phenotype and complement subnetwork molecular pathology without reducing A β burden. <i>Molecular Psychiatry</i> , 2019 , 24, 431-446	15.1	31
209	Integrative approach to sporadic Alzheimer's disease: deficiency of TYROBP in a tauopathy mouse model reduces C1q and normalizes clinical phenotype while increasing spread and state of phosphorylation of tau. <i>Molecular Psychiatry</i> , 2019 , 24, 1383-1397	15.1	26

208	STAR Chimeric Post for rapid detection of circular RNA and fusion transcripts. <i>Bioinformatics</i> , 2018 , 34, 2364-2370	7.2	16
207	Shared molecular neuropathology across major psychiatric disorders parallels polygenic overlap. <i>Science</i> , 2018 , 359, 693-697	33.3	547
206	Phase 2 Trial of Gemcitabine, Cisplatin, plus Ipilimumab in Patients with Metastatic Urothelial Cancer and Impact of DNA Damage Response Gene Mutations on Outcomes. <i>European Urology</i> , 2018 , 73, 751-759	10.2	67
205	Functional variants in the gene confer shared effects on risk for Crohn's disease and Parkinson's disease. <i>Science Translational Medicine</i> , 2018 , 10,	17.5	165
204	Integrated biology approach reveals molecular and pathological interactions among Alzheimer's A β 2, Tau, TREM2, and TYROBP in Drosophila models. <i>Genome Medicine</i> , 2018 , 10, 26	14.4	11
203	Genome Plasticity of -Defective Staphylococcus aureus during Clinical Infection. <i>Infection and Immunity</i> , 2018 , 86,	3.7	32
202	iPSC-derived familial Alzheimer's PSEN2 cholinergic neurons exhibit mutation-dependent molecular pathology corrected by insulin signaling. <i>Molecular Neurodegeneration</i> , 2018 , 13, 33	19	25
201	B Cell Defects Observed in Knockout Mice Are a Consequence of a Mutation Frequently Found in Inbred Strains. <i>Journal of Immunology</i> , 2018 , 201, 1442-1451	5.3	7
200	Impacts of incorporating personal genome sequencing into graduate genomics education: a longitudinal study over three course years. <i>BMC Medical Genomics</i> , 2018 , 11, 5	3.7	12
199	The human brainome: network analysis identifies HSPA2 as a novel Alzheimer's disease target. <i>Brain</i> , 2018 , 141, 2721-2739	11.2	19
198	A Nasal Brush-based Classifier of Asthma Identified by Machine Learning Analysis of Nasal RNA Sequence Data. <i>Scientific Reports</i> , 2018 , 8, 8826	4.9	33
197	Global analysis of A-to-I RNA editing reveals association with common disease variants. <i>PeerJ</i> , 2018 , 6, e4466	3.1	16
196	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. <i>Nature Genetics</i> , 2018 , 50, 524-537	36.3	536
195	The Mount Sinai cohort of large-scale genomic, transcriptomic and proteomic data in Alzheimer's disease. <i>Scientific Data</i> , 2018 , 5, 180185	8.2	144
194	Metagenomic binning and association of plasmids with bacterial host genomes using DNA methylation. <i>Nature Biotechnology</i> , 2018 , 36, 61-69	44.5	74
193	GJA1 (connexin43) is a key regulator of Alzheimer's disease pathogenesis. <i>Acta Neuropathologica Communications</i> , 2018 , 6, 144	7.3	37
192	Multiscale Analysis of Independent Alzheimer's Cohorts Finds Disruption of Molecular, Genetic, and Clinical Networks by Human Herpesvirus. <i>Neuron</i> , 2018 , 99, 64-82.e7	13.9	357
191	Functional regulatory mechanism of smooth muscle cell-restricted LMOD1 coronary artery disease locus. <i>PLoS Genetics</i> , 2018 , 14, e1007755	6	15

190	GWAS and colocalization analyses implicate carotid intima-media thickness and carotid plaque loci in cardiovascular outcomes. <i>Nature Communications</i> , 2018 , 9, 5141	17.4	64
189	Integrative transcriptome analyses of the aging brain implicate altered splicing in Alzheimer's disease susceptibility. <i>Nature Genetics</i> , 2018 , 50, 1584-1592	36.3	162
188	Temporal genetic association and temporal genetic causality methods for dissecting complex networks. <i>Nature Communications</i> , 2018 , 9, 3980	17.4	2
187	Detection of endometrial precancer by a targeted gynecologic cancer liquid biopsy. <i>Journal of Physical Education and Sports Management</i> , 2018 , 4,	2.8	7
186	Expression-based drug screening of neural progenitor cells from individuals with schizophrenia. <i>Nature Communications</i> , 2018 , 9, 4412	17.4	39
185	Mapping and characterizing N6-methyladenine in eukaryotic genomes using single-molecule real-time sequencing. <i>Genome Research</i> , 2018 , 28, 1067-1078	9.7	48
184	The asthma mobile health study, smartphone data collected using ResearchKit. <i>Scientific Data</i> , 2018 , 5, 180096	8.2	28
183	Melanocortin 4 Receptor Pathway Dysfunction in Obesity: Patient Stratification Aimed at MC4R Agonist Treatment. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2018 , 103, 2601-2612	5.6	31
182	From smartphone to EHR: a case report on integrating patient-generated health data. <i>Npj Digital Medicine</i> , 2018 , 1, 23	15.7	36
181	Psychological and behavioural impact of returning personal results from whole-genome sequencing: the HealthSeq project. <i>European Journal of Human Genetics</i> , 2017 , 25, 280-292	5.3	42
180	Heterozygous Pathogenic Variant in DACT1 Causes an Autosomal-Dominant Syndrome with Features Overlapping Townes-Brocks Syndrome. <i>Human Mutation</i> , 2017 , 38, 373-377	4.7	8
179	Rationale and Design of Family-Based Approach in a Minority Community Integrating Systems-Biology for Promotion of Health (FAMILIA). <i>American Heart Journal</i> , 2017 , 187, 170-181	4.9	10
178	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated With Coronary Artery Disease. <i>Journal of the American College of Cardiology</i> , 2017 , 69, 823-836	15.1	146
177	Deficiency of TYROBP, an adapter protein for TREM2 and CR3 receptors, is neuroprotective in a mouse model of early Alzheimer's pathology. <i>Acta Neuropathologica</i> , 2017 , 134, 769-788	14.3	55
176	Identification of a novel somatic mutation in a -mutated corticotroph adenoma. <i>Journal of Physical Education and Sports Management</i> , 2017 , 3, a001602	2.8	7
175	Directed Differentiation of Human Pluripotent Stem Cells to Microglia. <i>Stem Cell Reports</i> , 2017 , 8, 1516-1524	17.6	176
174	Large-Scale Identification of Common Trait and Disease Variants Affecting Gene Expression. <i>American Journal of Human Genetics</i> , 2017 , 100, 885-894	11	48
173	The Asthma Mobile Health Study, a large-scale clinical observational study using ResearchKit. <i>Nature Biotechnology</i> , 2017 , 35, 354-362	44.5	118

172	Analysis of Transcriptional Variability in a Large Human iPSC Library Reveals Genetic and Non-genetic Determinants of Heterogeneity. <i>Cell Stem Cell</i> , 2017 , 20, 518-532.e9	18	164
171	Human Pancreatic β Cell lncRNAs Control Cell-Specific Regulatory Networks. <i>Cell Metabolism</i> , 2017 , 25, 400-411	24.6	139
170	Insights into beta cell regeneration for diabetes via integration of molecular landscapes in human insulinomas. <i>Nature Communications</i> , 2017 , 8, 767	17.4	47
169	Institutional profile: translational pharmacogenomics at the Icahn School of Medicine at Mount Sinai. <i>Pharmacogenomics</i> , 2017 , 18, 1381-1386	2.6	13
168	Germline deletion of Krüppel-like factor 14 does not increase risk of diet induced metabolic syndrome in male C57BL/6 mice. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2017 , 1863, 3277-3285	6.9	12
167	Association of Body Mass Index with DNA Methylation and Gene Expression in Blood Cells and Relations to Cardiometabolic Disease: A Mendelian Randomization Approach. <i>PLoS Medicine</i> , 2017 , 14, e1002215	11.6	162
166	Multiscale network modeling of oligodendrocytes reveals molecular components of myelin dysregulation in Alzheimer's disease. <i>Molecular Neurodegeneration</i> , 2017 , 12, 82	19	61
165	Cancer gene profiling in non-small cell lung cancers reveals activating mutations in JAK2 and JAK3 with therapeutic implications. <i>Genome Medicine</i> , 2017 , 9, 89	14.4	23
164	CRISPR/Cas9-Correctable mutation-related molecular and physiological phenotypes in iPSC-derived Alzheimer's PSEN2 neurons. <i>Acta Neuropathologica Communications</i> , 2017 , 5, 77	7.3	73
163	Carbonyl reductase 1 catalyzes 20 β -reduction of glucocorticoids, modulating receptor activation and metabolic complications of obesity. <i>Scientific Reports</i> , 2017 , 7, 10633	4.9	11
162	A functional genomics predictive network model identifies regulators of inflammatory bowel disease. <i>Nature Genetics</i> , 2017 , 49, 1437-1449	36.3	107
161	Association analyses based on false discovery rate implicate new loci for coronary artery disease. <i>Nature Genetics</i> , 2017 , 49, 1385-1391	36.3	361
160	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. <i>Nature Communications</i> , 2017 , 8, 80	17.4	88
159	Biallelic Mutations in MRPS34 Lead to Instability of the Small Mitochondrial Subunit and Leigh Syndrome. <i>American Journal of Human Genetics</i> , 2017 , 101, 239-254	11	59
158	Integrative gene network analysis identifies key signatures, intrinsic networks and host factors for influenza virus A infections. <i>Npj Systems Biology and Applications</i> , 2017 , 3, 35	5	7
157	Integrative transcriptomic analysis reveals key drivers of acute peanut allergic reactions. <i>Nature Communications</i> , 2017 , 8, 1943	17.4	42
156	Gaining comprehensive biological insight into the transcriptome by performing a broad-spectrum RNA-seq analysis. <i>Nature Communications</i> , 2017 , 8, 59	17.4	130
155	A next generation sequencing based approach to identify extracellular vesicle mediated mRNA transfers between cells. <i>BMC Genomics</i> , 2017 , 18, 987	4.5	15

154	EXPLORING THE REPRODUCIBILITY OF PROBABILISTIC CAUSAL MOLECULAR NETWORK MODELS. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2017 , 22, 120-131	1.3	11
153	Genomic profiling reveals mutational landscape in parathyroid carcinomas. <i>JCI Insight</i> , 2017 , 2, e92061	9.9	50
152	Transcriptional dissection of melanoma identifies a high-risk subtype underlying TP53 family genes and epigenome deregulation. <i>JCI Insight</i> , 2017 , 2,	9.9	30
151	A phase I study of the safety and immunogenicity of a multi-peptide personalized genomic vaccine in the adjuvant treatment of solid cancers.. <i>Journal of Clinical Oncology</i> , 2017 , 35, TPS3114-TPS3114	2.2	4
150	High-Throughput Characterization of Blood Serum Proteomics of IBD Patients with Respect to Aging and Genetic Factors. <i>PLoS Genetics</i> , 2017 , 13, e1006565	6	30
149	Motivations, concerns and preferences of personal genome sequencing research participants: Baseline findings from the HealthSeq project. <i>European Journal of Human Genetics</i> , 2016 , 24, 14-20	5.3	64
148	Inferred miRNA activity identifies miRNA-mediated regulatory networks underlying multiple cancers. <i>Bioinformatics</i> , 2016 , 32, 96-105	7.2	21
147	Meditation and vacation effects have an impact on disease-associated molecular phenotypes. <i>Translational Psychiatry</i> , 2016 , 6, e880	8.6	50
146	Cardiometabolic risk loci share downstream cis- and trans-gene regulation across tissues and diseases. <i>Science</i> , 2016 , 353, 827-30	33.3	166
145	Integrative functional genomics identifies regulatory mechanisms at coronary artery disease loci. <i>Nature Communications</i> , 2016 , 7, 12092	17.4	70
144	Reconstructing Causal Network Models of Human Disease 2016 , 141-160		2
143	Discover the network underlying the connections between aging and age-related diseases. <i>Scientific Reports</i> , 2016 , 6, 32566	4.9	28
142	Identification of Altered Metabolomic Profiles Following a Panchakarma-based Ayurvedic Intervention in Healthy Subjects: The Self-Directed Biological Transformation Initiative (SBTI). <i>Scientific Reports</i> , 2016 , 6, 32609	4.9	20
141	Extensive sequencing of seven human genomes to characterize benchmark reference materials. <i>Scientific Data</i> , 2016 , 3, 160025	8.2	345
140	O2-06-01: The Human Brainome: Human Brain Genome, Transcriptome, and Proteome Integration 2016 , 12, P237-P238		1
139	F2-01-01: Oligodendrocyte-Enriched Gene Networks Reveal Novel Pathways and Key Targets in the Pathogenesis of Alzheimer's Disease 2016 , 12, P214-P214		
138	Integrative network analysis of nineteen brain regions identifies molecular signatures and networks underlying selective regional vulnerability to Alzheimer's disease. <i>Genome Medicine</i> , 2016 , 8, 104	14.4	135
137	variancePartition: interpreting drivers of variation in complex gene expression studies. <i>BMC Bioinformatics</i> , 2016 , 17, 483	3.6	201

136	Blood and Intestine eQTLs from an Anti-TNF-Resistant Crohn's Disease Cohort Inform IBD Genetic Association Loci. <i>Clinical and Translational Gastroenterology</i> , 2016 , 7, e177	4.2	21
135	Development and clinical application of an integrative genomic approach to personalized cancer therapy. <i>Genome Medicine</i> , 2016 , 8, 62	14.4	58
134	Cross-Tissue Regulatory Gene Networks in Coronary Artery Disease. <i>Cell Systems</i> , 2016 , 2, 196-208	10.6	81
133	exposures to environmental organic pollutants disrupt epigenetic marks linked to fetoplacental development. <i>Environmental Epigenetics</i> , 2016 , 2,	2.4	36
132	Molecular systems evaluation of oligomerogenic APP(E693Q) and fibrillogenic APP(KM670/671NL)/PSEN1(Δexon9) mouse models identifies shared features with human Alzheimer's brain molecular pathology. <i>Molecular Psychiatry</i> , 2016 , 21, 1099-111	15.1	8
131	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. <i>Nature Communications</i> , 2016 , 7, 10495	17.4	180
130	Variants in TRIM22 That Affect NOD2 Signaling Are Associated With Very-Early-Onset Inflammatory Bowel Disease. <i>Gastroenterology</i> , 2016 , 150, 1196-1207	13.3	69
129	Impact of Genomic Counseling on Informed Decision-Making among ostensibly Healthy Individuals Seeking Personal Genome Sequencing: the HealthSeq Project. <i>Journal of Genetic Counseling</i> , 2016 , 25, 1044-53	2.5	14
128	A Next Generation Multiscale View of Inborn Errors of Metabolism. <i>Cell Metabolism</i> , 2016 , 23, 13-26	24.6	55
127	Transgenic drosophila as a drug-screening platform in colorectal cancer and medullary thyroid cancer.. <i>Journal of Clinical Oncology</i> , 2016 , 34, e23164-e23164	2.2	2
126	Continuous Surveillance by Whole-Genome Sequencing to Identify and Manage Methicillin-Resistant Staphylococcus aureus Outbreaks. <i>Open Forum Infectious Diseases</i> , 2016 , 3,	1	1
125	S4-02-03: Accelerating Medicines Partnership: Co-Expression Networks 2016 , 12, P322-P322		
124	P4-027: Combing Evidence Across Multiple Cohorts for Systems-Based Target Discovery: the AMP-AD Knowledge Portal 2016 , 12, P1025-P1025		
123	P4-031: Integrative Network Analysis of Multiple Alzheimer's Disease Rnaseq Studies From the Accelerating Medicine Partnership-Alzheimer's Disease Consortium 2016 , 12, P1026-P1027		1
122	P4-278: Characterization of Basal Forebrain Cholinergic Neurons From Induced Pluripotent Stem Cells Harboring Familial Alzheimer's MUTATION PSEN2 N141I 2016 , 12, P1139-P1139		
121	Family-Based Approaches to Cardiovascular Health Promotion. <i>Journal of the American College of Cardiology</i> , 2016 , 67, 1725-37	15.1	40
120	A new molecular signature method for prediction of driver cancer pathways from transcriptional data. <i>Nucleic Acids Research</i> , 2016 , 44, e110	20.1	11
119	Analysis of 589,306 genomes identifies individuals resilient to severe Mendelian childhood diseases. <i>Nature Biotechnology</i> , 2016 , 34, 531-8	44.5	196

118	Gene expression elucidates functional impact of polygenic risk for schizophrenia. <i>Nature Neuroscience</i> , 2016 , 19, 1442-1453	25.5	622
117	Decision-Making in the Age of Whole Genome Sequencing 2016 , 357-373		
116	Genome-wide significant loci: how important are they? Systems genetics to understand heritability of coronary artery disease and other common complex disorders. <i>Journal of the American College of Cardiology</i> , 2015 , 65, 830-845	15.1	108
115	Genomic and network patterns of schizophrenia genetic variation in human evolutionary accelerated regions. <i>Molecular Biology and Evolution</i> , 2015 , 32, 1148-60	8.3	60
114	Single molecule-level detection and long read-based phasing of epigenetic variations in bacterial methylomes. <i>Nature Communications</i> , 2015 , 6, 7438	17.4	64
113	Integrative analysis of DNA methylation and gene expression data identifies EPAS1 as a key regulator of COPD. <i>PLoS Genetics</i> , 2015 , 11, e1004898	6	54
112	Assembly and diploid architecture of an individual human genome via single-molecule technologies. <i>Nature Methods</i> , 2015 , 12, 780-6	21.6	383
111	An integrated map of structural variation in 2,504 human genomes. <i>Nature</i> , 2015 , 526, 75-81	50.4	1368
110	Genome-wide identification of microRNAs regulating cholesterol and triglyceride homeostasis. <i>Nature Medicine</i> , 2015 , 21, 1290-7	50.5	160
109	Preparing the next generation of genomicists: a laboratory-style course in medical genomics. <i>BMC Medical Genomics</i> , 2015 , 8, 47	3.7	14
108	Integrative genomics identifies 7p11.2 as a novel locus for fever and clinical stress response in humans. <i>Human Molecular Genetics</i> , 2015 , 24, 1801-12	5.6	16
107	A robust blood gene expression-based prognostic model for castration-resistant prostate cancer. <i>BMC Medicine</i> , 2015 , 13, 201	11.4	12
106	Whole-genome sequencing identifies emergence of a quinolone resistance mutation in a case of <i>Stenotrophomonas maltophilia</i> bacteremia. <i>Antimicrobial Agents and Chemotherapy</i> , 2015 , 59, 7117-20	5.9	16
105	Prediction of Causal Candidate Genes in Coronary Artery Disease Loci. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2015 , 35, 2207-17	9.4	64
104	Deciphering H3K4me3 broad domains associated with gene-regulatory networks and conserved epigenomic landscapes in the human brain. <i>Translational Psychiatry</i> , 2015 , 5, e679	8.6	42
103	Systems biology of asthma and allergic diseases: a multiscale approach. <i>Journal of Allergy and Clinical Immunology</i> , 2015 , 135, 31-42	11.5	91
102	Modern Methods for Delineating Metagenomic Complexity. <i>Cell Systems</i> , 2015 , 1, 6-7	10.6	13
101	Synchronized age-related gene expression changes across multiple tissues in human and the link to complex diseases. <i>Scientific Reports</i> , 2015 , 5, 15145	4.9	128

100	Personalized Circulating Tumor DNA Biomarkers Dynamically Predict Treatment Response and Survival In Gynecologic Cancers. <i>PLoS ONE</i> , 2015 , 10, e0145754	3.7	97
99	Novel, compound heterozygous, single-nucleotide variants in MARS2 associated with developmental delay, poor growth, and sensorineural hearing loss. <i>Human Mutation</i> , 2015 , 36, 587-92	4.7	21
98	Geospatial Resolution of Human and Bacterial Diversity with City-Scale Metagenomics. <i>Cell Systems</i> , 2015 , 1, 72-87	10.6	164
97	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015 , 518, 187-196	50.4	920
96	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015 , 518, 197-206	50.4	2687
95	Massive parallel sequencing uncovers actionable FGFR2-PPHLN1 fusion and ARAF mutations in intrahepatic cholangiocarcinoma. <i>Nature Communications</i> , 2015 , 6, 6087	17.4	183
94	How do students react to analyzing their own genomes in a whole-genome sequencing course?: outcomes of a longitudinal cohort study. <i>Genetics in Medicine</i> , 2015 , 17, 866-74	8.1	25
93	Causal inference in biology networks with integrated belief propagation. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2015 , 359-70	1.3	7
92	Genomic analysis and personalized cancer therapy for metastatic colorectal cancer.. <i>Journal of Clinical Oncology</i> , 2015 , 33, 568-568	2.2	
91	Patient-Specific Mutation-Derived Tumor Antigens As Targets for Cancer Immunotherapy in Multiple Myeloma. <i>Blood</i> , 2015 , 126, 1851-1851	2.2	
90	Translational genomics. Clues from the resilient. <i>Science</i> , 2014 , 344, 970-2	33.3	33
89	Geroscience: linking aging to chronic disease. <i>Cell</i> , 2014 , 159, 709-13	56.2	1068
88	iPSC-derived dopamine neurons reveal differences between monozygotic twins discordant for Parkinson's disease. <i>Cell Reports</i> , 2014 , 9, 1173-82	10.6	166
87	Common dysregulation network in the human prefrontal cortex underlies two neurodegenerative diseases. <i>Molecular Systems Biology</i> , 2014 , 10, 743	12.2	101
86	A data driven approach to diagnosing and treating disease 2014 ,		1
85	The role of macromolecular damage in aging and age-related disease. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2014 , 69 Suppl 1, S28-32	6.4	38
84	Lim domain binding 2: a key driver of transendothelial migration of leukocytes and atherosclerosis. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2014 , 34, 2068-77	9.4	12
83	Integrated genome-wide association, coexpression network, and expression single nucleotide polymorphism analysis identifies novel pathway in allergic rhinitis. <i>BMC Medical Genomics</i> , 2014 , 7, 48	3.7	45

82	lrgpr: interactive linear mixed model analysis of genome-wide association studies with composite hypothesis testing and regression diagnostics in R. <i>Bioinformatics</i> , 2014 , 30, 3134-5	7.2	9
81	Analytical validation of whole exome and whole genome sequencing for clinical applications. <i>BMC Medical Genomics</i> , 2014 , 7, 20	3.7	82
80	Downregulation of carnitine acyl-carnitine translocase by miRNAs 132 and 212 amplifies glucose-stimulated insulin secretion. <i>Diabetes</i> , 2014 , 63, 3805-14	0.9	40
79	Personalized ovarian cancer disease surveillance and detection of candidate therapeutic drug target in circulating tumor DNA. <i>Neoplasia</i> , 2014 , 16, 97-103	6.4	40
78	Causal effects of body mass index on cardiometabolic traits and events: a Mendelian randomization analysis. <i>American Journal of Human Genetics</i> , 2014 , 94, 198-208	11	156
77	Biomarkers for combat-related PTSD: focus on molecular networks from high-dimensional data. <i>Hjgre Utbildning</i> , 2014 , 5,	5	17
76	TGF β receptor 1: an immune susceptibility gene in HPV-associated cancer. <i>Cancer Research</i> , 2014 , 74, 6833-44	10.1	29
75	A role for noncoding variation in schizophrenia. <i>Cell Reports</i> , 2014 , 9, 1417-29	10.6	174
74	Dissection of immune gene networks in primary melanoma tumors critical for antitumor surveillance of patients with stage II-III resectable disease. <i>Journal of Investigative Dermatology</i> , 2014 , 134, 2202-2211	4.3	42
73	Bayesian test for colocalisation between pairs of genetic association studies using summary statistics. <i>PLoS Genetics</i> , 2014 , 10, e1004383	6	868
72	MODMatcher: multi-omics data matcher for integrative genomic analysis. <i>PLoS Computational Biology</i> , 2014 , 10, e1003790	5	25
71	Evolving toward a human-cell based and multiscale approach to drug discovery for CNS disorders. <i>Frontiers in Pharmacology</i> , 2014 , 5, 252	5.6	31
70	Autotransporters but not pAA are critical for rabbit colonization by Shiga toxin-producing <i>Escherichia coli</i> O104:H4. <i>Nature Communications</i> , 2014 , 5, 3080	17.4	32
69	Gene-centric meta-analysis in 87,736 individuals of European ancestry identifies multiple blood-pressure-related loci. <i>American Journal of Human Genetics</i> , 2014 , 94, 349-60	11	131
68	Mutations in tetratricopeptide repeat domain 7A result in a severe form of very early onset inflammatory bowel disease. <i>Gastroenterology</i> , 2014 , 146, 1028-39	13.3	138
67	Large-scale association analysis identifies new risk loci for coronary artery disease. <i>Nature Genetics</i> , 2013 , 45, 25-33	36.3	1172
66	CR1 and the "vanishing amyloid" hypothesis of Alzheimer's disease. <i>Biological Psychiatry</i> , 2013 , 73, 393-57.9		18
65	Causal Inference and the Construction of Predictive Network Models in Biology 2013 , 499-514		1

64	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. <i>Nature Genetics</i> , 2013 , 45, 501-12	36.3	437
63	Integrated systems approach identifies genetic nodes and networks in late-onset Alzheimer's disease. <i>Cell</i> , 2013 , 153, 707-20	56.2	1058
62	Modeling kinetic rate variation in third generation DNA sequencing data to detect putative modifications to DNA bases. <i>Genome Research</i> , 2013 , 23, 129-41	9.7	63
61	Detecting DNA modifications from SMRT sequencing data by modeling sequence context dependence of polymerase kinetic. <i>PLoS Computational Biology</i> , 2013 , 9, e1002935	5	44
60	Comprehensive methylome characterization of <i>Mycoplasma genitalium</i> and <i>Mycoplasma pneumoniae</i> at single-base resolution. <i>PLoS Genetics</i> , 2013 , 9, e1003191	6	75
59	Informed decision-making among students analyzing their personal genomes on a whole genome sequencing course: a longitudinal cohort study. <i>Genome Medicine</i> , 2013 , 5, 113	14.4	25
58	Bayesian method to predict individual SNP genotypes from gene expression data. <i>Nature Genetics</i> , 2012 , 44, 603-8	36.3	108
57	Genome-wide mapping of methylated adenine residues in pathogenic <i>Escherichia coli</i> using single-molecule real-time sequencing. <i>Nature Biotechnology</i> , 2012 , 30, 1232-9	44.5	256
56	Host-microbe interactions have shaped the genetic architecture of inflammatory bowel disease. <i>Nature</i> , 2012 , 491, 119-24	50.4	3239
55	Genetics. A GPS for navigating DNA. <i>Science</i> , 2012 , 337, 1179-80	33.3	4
54	This I believe: gaining new insights through integrating "old" data. <i>Frontiers in Genetics</i> , 2012 , 3, 137	4.5	8
53	A hybrid approach for the automated finishing of bacterial genomes. <i>Nature Biotechnology</i> , 2012 , 30, 701-707	44.5	157
52	Stitching together multiple data dimensions reveals interacting metabolomic and transcriptomic networks that modulate cell regulation. <i>PLoS Biology</i> , 2012 , 10, e1001301	9.7	142
51	Integrative analysis of a cross-loci regulation network identifies App as a gene regulating insulin secretion from pancreatic islets. <i>PLoS Genetics</i> , 2012 , 8, e1003107	6	49
50	NEW: network-enabled wisdom in biology, medicine, and health care. <i>Science Translational Medicine</i> , 2012 , 4, 115rv1	17.5	97
49	Leveraging models of cell regulation and GWAS data in integrative network-based association studies. <i>Nature Genetics</i> , 2012 , 44, 841-7	36.3	198
48	Systems analysis of eleven rodent disease models reveals an inflammatome signature and key drivers. <i>Molecular Systems Biology</i> , 2012 , 8, 594	12.2	95
47	Origins of the <i>E. coli</i> strain causing an outbreak of hemolytic-uremic syndrome in Germany. <i>New England Journal of Medicine</i> , 2011 , 365, 709-17	59.2	658

46	Predictive genes in adjacent normal tissue are preferentially altered by sCNV during tumorigenesis in liver cancer and may rate limiting. <i>PLoS ONE</i> , 2011 , 6, e20090	3.7	51
45	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. <i>American Journal of Human Genetics</i> , 2011 , 88, 6-18	11	103
44	Inferring causal genomic alterations in breast cancer using gene expression data. <i>BMC Systems Biology</i> , 2011 , 5, 121	3.5	46
43	A survey of the genetics of stomach, liver, and adipose gene expression from a morbidly obese cohort. <i>Genome Research</i> , 2011 , 21, 1008-16	9.7	141
42	The origin of the Haitian cholera outbreak strain. <i>New England Journal of Medicine</i> , 2011 , 364, 33-42	59.2	559
41	From noncoding variant to phenotype via SORT1 at the 1p13 cholesterol locus. <i>Nature</i> , 2010 , 466, 714-9	50.4	820
40	Biological, clinical and population relevance of 95 loci for blood lipids. <i>Nature</i> , 2010 , 466, 707-13	50.4	2742
39	Hundreds of variants clustered in genomic loci and biological pathways affect human height. <i>Nature</i> , 2010 , 467, 832-8	50.4	1514
38	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. <i>Nature Genetics</i> , 2010 , 42, 949-60	36.3	724
37	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. <i>Nature Genetics</i> , 2010 , 42, 937-48	36.3	2267
36	The effect of food intake on gene expression in human peripheral blood. <i>Human Molecular Genetics</i> , 2010 , 19, 159-69	5.6	39
35	Systematic genetic and genomic analysis of cytochrome P450 enzyme activities in human liver. <i>Genome Research</i> , 2010 , 20, 1020-36	9.7	193
34	An integration of genome-wide association study and gene expression profiling to prioritize the discovery of novel susceptibility Loci for osteoporosis-related traits. <i>PLoS Genetics</i> , 2010 , 6, e1000977	6	163
33	A Bayesian partition method for detecting pleiotropic and epistatic eQTL modules. <i>PLoS Computational Biology</i> , 2010 , 6, e1000642	5	55
32	Characterizing dynamic changes in the human blood transcriptional network. <i>PLoS Computational Biology</i> , 2010 , 6, e1000671	5	50
31	Liver and adipose expression associated SNPs are enriched for association to type 2 diabetes. <i>PLoS Genetics</i> , 2010 , 6, e1000932	6	139
30	A window into third-generation sequencing. <i>Human Molecular Genetics</i> , 2010 , 19, R227-40	5.6	628
29	Integrating pathway analysis and genetics of gene expression for genome-wide association studies. <i>American Journal of Human Genetics</i> , 2010 , 86, 581-91	11	202

28	Genetic validation of whole-transcriptome sequencing for mapping expression affected by cis-regulatory variation. <i>BMC Genomics</i> , 2010 , 11, 473	4.5	27
27	Magnitude of stratification in human populations and impacts on genome wide association studies. <i>PLoS ONE</i> , 2010 , 5, e8695	3.7	12
26	Ppargamma2 is a key driver of longevity in the mouse. <i>PLoS Genetics</i> , 2009 , 5, e1000752	6	62
25	Integrating siRNA and protein-protein interaction data to identify an expanded insulin signaling network. <i>Genome Research</i> , 2009 , 19, 1057-67	9.7	45
24	Molecular networks as sensors and drivers of common human diseases. <i>Nature</i> , 2009 , 461, 218-23	50.4	589
23	Validation of candidate causal genes for obesity that affect shared metabolic pathways and networks. <i>Nature Genetics</i> , 2009 , 41, 415-23	36.3	224
22	A network view of disease and compound screening. <i>Nature Reviews Drug Discovery</i> , 2009 , 8, 286-95	64.1	219
21	Multi-tissue coexpression networks reveal unexpected subnetworks associated with disease. <i>Genome Biology</i> , 2009 , 10, R55	18.3	121
20	Disentangling molecular relationships with a causal inference test. <i>BMC Genetics</i> , 2009 , 10, 23	2.6	163
19	Variations in DNA elucidate molecular networks that cause disease. <i>Nature</i> , 2008 , 452, 429-35	50.4	723
18	Genetics of gene expression and its effect on disease. <i>Nature</i> , 2008 , 452, 423-8	50.4	1058
17	Integrating large-scale functional genomic data to dissect the complexity of yeast regulatory networks. <i>Nature Genetics</i> , 2008 , 40, 854-61	36.3	430
16	Mapping the genetic architecture of gene expression in human liver. <i>PLoS Biology</i> , 2008 , 6, e107	9.7	768
15	Moving toward a system genetics view of disease. <i>Mammalian Genome</i> , 2007 , 18, 389-401	3.2	148
14	Increasing the power to detect causal associations by combining genotypic and expression data in segregating populations. <i>PLoS Computational Biology</i> , 2007 , 3, e69	5	156
13	Tissue-specific expression and regulation of sexually dimorphic genes in mice. <i>Genome Research</i> , 2006 , 16, 995-1004	9.7	628
12	Elucidating the murine brain transcriptional network in a segregating mouse population to identify core functional modules for obesity and diabetes. <i>Journal of Neurochemistry</i> , 2006 , 97 Suppl 1, 50-62	6	78
11	An integrative genomics approach to infer causal associations between gene expression and disease. <i>Nature Genetics</i> , 2005 , 37, 710-7	36.3	820

10	Cis-acting expression quantitative trait loci in mice. <i>Genome Research</i> , 2005 , 15, 681-91	9.7	216
9	An integrative genomics approach to the reconstruction of gene networks in segregating populations. <i>Cytogenetic and Genome Research</i> , 2004 , 105, 363-74	1.9	178
8	Genetics of gene expression surveyed in maize, mouse and man. <i>Nature</i> , 2003 , 422, 297-302	50.4	1244
7	Experimental annotation of the human genome using microarray technology. <i>Nature</i> , 2001 , 409, 922-7	50.4	373
6	Integrative transcriptome imputation reveals tissue-specific and shared biological mechanisms mediating susceptibility to complex traits		1
5	Intestinal inflammation modulates the expression of ACE2 and TMPRSS2 and potentially overlaps with the pathogenesis of SARS-CoV-2 related disease		7
4	Single Cell-type Integrative Network Modeling Identified Novel Microglial-specific Targets for the Phagosome in Alzheimer's disease		1
3	Multiscale causal network models of Alzheimer's disease identify VGF as a key regulator of disease		4
2	Meta-analysis of the human brain transcriptome identifies heterogeneity across human AD coexpression modules robust to sample collection and methodological approach		14
1	Molecular Networks and Key Regulators of the Dysregulated Neuronal System in Alzheimer's Disease		1